



DNA methylation in embryonic stem cells.

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Public Summary:

Embryonic stem cells (ESCs) are pluripotent, self-renewing cells. These cells can be used in applications such as cell therapy, drug development, disease modeling, and the study of cellular differentiation. Investigating the interplay of epigenetics, genetics, and gene expression in control of pluripotence and differentiation could give important insights on how these cells function.

Scientific Abstract:

Embryonic stem cells (ESCs) are pluripotent, self-renewing cells. These cells can be used in applications such as cell therapy, drug development, disease modeling, and the study of cellular differentiation. Investigating the interplay of epigenetics, genetics, and gene expression in control of pluripotence and differentiation could give important insights on how these cells function. One of the best known epigenetic factors is DNA methylation, which is a major mechanism for regulation of gene expression. This phenomenon is mostly seen in imprinted genes and X-chromosome inactivation where DNA methylation of promoter regions leads to repression of gene expression. Differential DNA methylation of pluripotence-associated genes such as Nanog and Oct4/Pou5f1 has been observed between pluripotent and differentiated cells. It is clear that tight regulation of DNA methylation is necessary for normal development. As more associations between aberrant DNA methylation and disease are reported, the demand for high-throughput approaches for DNA methylation analysis has increased. In this article, we highlight these methods and discuss recent DNA methylation studies on ESCs.

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